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☐ 1: 2006271A. Reports Phe ammonia lyase...[gi:741010]

BLink, Domains,
Links

LOCUS 2006271A 725 aa linear PLN 10-JUL-1992
 DEFINITION Phe ammonia lyase.
 ACCESSION 2006271A
 VERSION 2006271A GI:741010
 DBSOURCE prf: locus 2006271A;

state: embryo;
 taxonomy: Plantae.
 KEYWORDS Phe Ammonia Lyase; Trifolium subterraneum; PAL1 Gene;
 Acc.No.M91192; PCR Amplification; AAAIMEHI; EQHNQDV; Seq
 Determination; 3300bp; 725AAs; DNA Blot; Multigene Family.
 SOURCE Trifolium subterraneum
 ORGANISM Trifolium subterraneum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Trifolium.

REFERENCE 1 (residues 1 to 725)
 AUTHORS Howles,P.A., Arioli,T. and Weinman,J.J.
 TITLE Characterization of a phenylalanine ammonia-lyase multigene family
 in Trifolium subterraneum
 JOURNAL Gene 138(1/2), 87-92 (1994)
 COMMENT EC=2.3.1.74:GENE=PAL1.
 FEATURES Location/Qualifiers
 source 1..725
 /organism="Trifolium subterraneum"
 /db_xref="taxon:3900"

ORIGIN

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1 mevvaailk nnindydsfc lthanannmk vnaadplnwg vaaeamkgsh ldevkrmvee
61 yrkpvvrlgg etltisqvaa iaahdgatve lsesaragvk assdwvmesm nkgtdsygvt
121 tgfgatshrr tkqggalqke lirflnagif gngtesnhtl fhtatraaml vrintllggy
181 sgirfeilea itklennnit pclplrgtit asgdlvplsy iaglltgpsn skahgpgsem
241 lnakeafqla ginaeffelq pkeglalvng tavgsglasi vlfeanilav lsevlsaifa
301 evmqgkpeft dhlthklkhh pgqieaaaam ehilhgsayv kdakklhemd plqkpkqdry
361 alrtspqwlq plievirfst ksiereinsv ndnplidvsr nkalhggnfq gtpigvsmnd
421 trlalasigk llfaqfselv ndfynnglps nlsasrnpsl dygfgkseia masycselqy
481 lanpvtthvq saeqhnqdv nslglissrkt keaieilqlm sstflialcq aidlrhleen
541 lknsvkntvs qvakktltig vsgehlpsrf cekd1lkvvd rehvfisyidd pcsatyplaq
601 klrqvlvdha lvngesekns ntsifqkiat feeelktllp kevesartay engnstiank
661 ingcrsypl ykfvreelgts lltgervisp geedklfta mcqgkiidpl lklclgewnga
721 plpic

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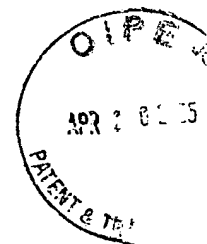
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Range: from to
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 ☒ MGC
 ☐ HPRD
 ☐ STS

☐ 1: [P45726](#). Reports Phenylalanine amm...[gi:1171998]

[BLink](#), [Domains](#),
[Links](#)

LOCUS P45726 714 aa linear PLN 01-MAY-2005
 DEFINITION Phenylalanine ammonia-lyase.
 ACCESSION P45726
 VERSION P45726 GI:1171998
 DBSOURCE swissprot: locus PALY_CAMSI, accession [P45726](#);
 class: standard.
 created: Nov 1, 1995.
 sequence updated: Nov 1, 1995.
 annotation updated: May 1, 2005.
 xrefs: [D26596.1](#), [BAA05643.1](#)
 xrefs (non-sequence databases): [HSSPP21310](#), [InterProIPR008948](#),
[InterProIPR001106](#), [InterProIPR005922](#), [PfamPF00221](#),
[TIGRFAMsTIGR01226](#), [PROSITEPS00488](#)
 KEYWORDS Lyase; Phenylpropanoid metabolism.
 SOURCE *Camellia sinensis* (black tea)
 ORGANISM *Camellia sinensis*
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; Ericales; Theaceae; *Camellia*.
 REFERENCE 1 (residues 1 to 714)
 AUTHORS Matsumoto,S., Takeuchi,A., Hayatsu,M. and Kondo,S.
 TITLE Molecular cloning of phenylalanine ammonia-lyase cDNA and
 classification of varieties and cultivars of tea plants (*Camellia*
sinensis) using the tea PAL cDNA probe
 JOURNAL Theor. Appl. Genet. 89, 671-675 (1994)
 REMARK NUCLEOTIDE SEQUENCE.
 STRAIN=cv. Yabukita; TISSUE=Leaf
 COMMENT [FUNCTION] This is a key enzyme of plant metabolism catalyzing the
 first reaction in the biosynthesis from L-phenylalanine of a wide
 variety of natural products based on the phenylpropane skeleton.
 [CATALYTIC ACTIVITY] L-phenylalanine = trans-cinnamate + NH(3).
 [PATHWAY] Phenylpropanoid biosynthesis; first step.
 [SUBCELLULAR LOCATION] Cytoplasmic (Probable).
 [PTM] Contains an active site 4-methylidene-imidazole-5-one (MIO),
 which is formed autocatalytically by cyclization and dehydration of
 residues Ala-Ser-Gly (By similarity).
 [SIMILARITY] Belongs to the PAL/histidase family.
 FEATURES
 Location/Qualifiers
 source 1..714
 /organism="Camellia sinensis"
 /db_xref="taxon:4442"
 gene 1..714
 /gene="PAL"
 Protein 1..714
 /gene="PAL"



Bond /product="Phenylalanine ammonia-lyase"
/EC_number="4.3.1.5"
bond(200,202)
/gene="PAL"
/bond_type="xlink"
/note="5-imidazolinone (Ala-Gly) (By similarity)."
/evidence=not_experimental

Site 201
/gene="PAL"
/site_type="modified"
/note="2,3-didehydroalanine (Ser) (By similarity)."
/evidence=not_experimental




ORIGIN

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1 mdsttaigng vsgggspgfc lkdplnwgva aeamkgshle evkgmveefr kpvvrlgget
61 ltisqvaaia vrgsevavel sesaregvka ssdwvmesmn kgtdsygvtt gfgatshrtr
121 keggalqkel irflnagifg ngteschtlp qsatraamlv rintllqgys girfeileai
181 skflnnnitp clplrgtita sgdlvplsyi aglltgrhns kavgptgeil hpkeafrlag
241 veggffelqp keglalvngt avsgglasmv lfeanilavl sevlsaifae vmggkpeftd
301 hlthklkhhp gqieaaaime hildgssyvk aaqklhemdp lqkpkqdrya lrtspqwlgp
361 lievirsstk siereinsvn dnplnvsrn kalhggnfqg tpigvsmndt rlavasigkl
421 mfaqfselvn dfynnglpsn lsggrnpsld ygfkgaieam aaycselqfl anpvtnhvsq
481 aeghnqdvns lgliissrkta eavdilklms stylvalcqa vdlrhfeenl rntvkstvsq
541 vakrvltmgv ngelhpsrhc ekdlrrvvdv eyifayiddp csatyplmqk lrqvlvehal
601 kngeseknls tsifqkiraf eeeiktllpk evestraaie ngnsaipnri kecrsyplyk
661 fvreelgtel ltgekvrspg eefdkvftal ckgemidplm dclkewngap lpic
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☐ 1: [CAA68938](#). Reports PAL1 protein [Pet...[gi:1524313]

BLink, Domains,
Links

LOCUS CAA68938 716 aa linear PLN 02-SEP-1996
 DEFINITION PAL1 protein [Petroselinum crispum].
 ACCESSION CAA68938
 VERSION CAA68938.1 GI:1524313
 DBSOURCE embl locus PCPAL1, accession [Y07654.1](#)
 KEYWORDS
 SOURCE Petroselinum crispum (parsley)
 ORGANISM Petroselinum crispum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; campanulids; Apiales; Apiaceae; Apioideae; apioid
 superclade; Apium clade; Petroselinum.
 REFERENCE 1
 AUTHORS Kang,X., Logemann,E. and Hahlbrock,K.
 TITLE Cis-acting elements of the parsley pal1 gene
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 716)
 AUTHORS Kang,X.
 TITLE Direct Submission
 JOURNAL Submitted (27-AUG-1996) X. Kang, Max-Planck-Institut, Biochemistry,
 Carl-von-Linne-Weg 10, 50829 Cologne, FRG
 COMMENT Related sequences X16772 (exon2), and X15473 (5'UTR and exon1).
 FEATURES Location/Qualifiers
 source 1..716
 /organism="Petroselinum crispum"
 /db_xref="taxon:4043"
 /clone="xk-Pcpall"
 /cell_line="Pc-5 /5"
 /tissue_type="cell suspension"
 Protein 1..716
 /product="PAL1 protein"
 CDS 1..716
 /gene="pal1 gene"
 /coded_by="join(Y07654.1:1969..2375,Y07654.1:3169..4912)"
 /db_xref="GOA:P24481"
 /db_xref="UniProt/Swiss-Prot:[P24481](#)"

ORIGIN

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1  mengngattn ghvngngmdf cmktdedplyw giaaeamtgs hldevkkmva eyrkpvvklg
61  getltisqva aisardgsgv tvelseaara gvkassdwvm dsmnkgtdsy gvtgtfgats
121 hrrtkqggal qkelirflna gifngsdnt lphsatraam lvrintl1qg ysgirfeile
181 aitkflnqni tpclplrgti tasgdlvpls yiaglltgrp nskavgptgv ilspeeafkl
241 agveggffef qpkeglalvn gtavsgsmas mvlfeanila vlaevmsaif aevmqgkpef
301 tdhlthklkh hpggieaaai mehildgsay vkaaqlhem dplqkpkqdr yalrtspqwl
361 gpgievirss tkmiereins vndnplidvs rnkaihggnf qgtpigvsm d ntrlaiaaig
421 klmfaqfsel vndfynnglp snlsggrnps ldygfkgaie amasytselq flnppvtnhv



```

481 qsaeqhnqdv nslglissrk tseaveilk1 msttflvglc qaidlrhlee nlkstvkntv
541 ssvakrvltm gvngelhpsr fcekdllrvv dreyifayid dpcsatyp1m qklrqt1veh
601 alknqdnern lstsifqkia tfedelkall pkevesaraa lesnpaipn rieecrsypl
661 ykfvrkelgt eyltgekvts pgeefekvfi amskgeiidp llecleswng aplpic

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☐ 1: [AAG49585](#). Reports phenylalanine amm...[gi:12240240]

BLink, Domains,
Links

LOCUS AAG49585 711 aa linear PLN 16-JAN-2001
 DEFINITION phenylalanine ammonia-lyase [Ipomoea nil].
 ACCESSION AAG49585
 VERSION AAG49585.1 GI:12240240
 DBSOURCE locus AF325496 accession [AF325496.1](#)
 KEYWORDS .
 SOURCE Ipomoea nil (Japanese morning glory)
 ORGANISM Ipomoea nil
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiids; Solanales; Convolvulaceae; Ipomoeae; Ipomoea.
 REFERENCE 1 (residues 1 to 711)
 AUTHORS Nakazawa,A., Nozue,M., Yasuda,H., Takeba,G. and Kubo,H.
 TITLE Expression of phenylalanine ammonia-lyase in Pharbitis nil
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 711)
 AUTHORS Nakazawa,A., Nozue,M., Yasuda,H., Takeba,G. and Kubo,H.
 TITLE Direct Submission
 JOURNAL Submitted (01-DEC-2000) Biology, Shinshu University, Asahi 3-1-1,
 Matsumoto 390-8621, Japan
 COMMENT Method: conceptual translation supplied by author.
 FEATURES Location/Qualifiers
 source 1..711
 /organism="Ipomoea nil"
 /cultivar="Violet"
 /db_xref="taxon:35883"
 Protein 1..711
 /product="phenylalanine ammonia-lyase"
 /EC_number="4.3.1.5"
 CDS 1..711
 /coded_by="join(AF325496.1:1034..1419,
 AF325496.1:2409..4158) "

ORIGIN

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1 mdsvklqngg hqngfcvkvd plnwevaads lrgshldevk vmvaefrkpa vklggetltv
61 aqvaaiasrd navtvelsee sragvkassd wvmdsmnkgd dsygvttgfg atshrrtkgg
121 galqkelirf lnagifngt eschtlphsa traamlvrin tllqgysgir feileaitkl
181 lnhnitpcpl lrgtitasgd lvplsyiagl itgrpnskav gpngetlnae ealrlagvng
241 gffelqpkeg lalvngtavg sgmasmvife anvlavlsev lsaifaevmn gkpeftdhlt
301 hklkhpggqi eaaaimihil dgssyvkaa qkmhemdplqk pkqdryalrt spqwlgpqie
361 viraatkmi reinsvndnp lidvarskal hggngfggtpi gvsmndsrln lasigklfla
421 qfselvndyy nnglpsnlta grnpsldygf kgaaiamasy cselqlanp vtnhvtqsaq
481 hnqdvnsllg lsarktaeav dvlklmssty lvalcqaidl rfleenlrna vknavtqvak
541 rltltmgange lhparfcked llrvvdreyv fayaddpcsa nyplmqklrq alvdhalqng
601 esekntgtst flkvaafede lkavlpkeve aariavesgn paipnriec rsyplykfvr
661 eglgtelltg ekvrspgeec dkvftamceg siidpllecl kswdgaplpi c

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☐ 1: [AAL55242](#). Reports phenylalanine amm...[gi:18001007]

BLink, Domains,
Links

LOCUS AAL55242 711 aa linear PLN_01-MAR-2005
 DEFINITION phenylalanine ammonia-lyase [*Lactuca sativa*].
 ACCESSION AAL55242
 VERSION AAL55242.1 GI:18001007
 DBSOURCE accession [AF299330.1](#)
 KEYWORDS
 SOURCE *Lactuca sativa*
 ORGANISM *Lactuca sativa*
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
 Cichorieae; *Lactuca*.
 REFERENCE 1 (residues 1 to 711)
 AUTHORS Campos,R., Nonogaki,H., Suslow,T. and Saltveit,M.E.
 TITLE Isolation and characterization of a wound inducible phenylalanine
 ammonia-lyase gene (LsPAL1) from Romaine lettuce leaves
 JOURNAL Physiol. Plantarum 121 (3), 429-438 (2004)
 REFERENCE 2 (residues 1 to 711)
 AUTHORS Campos-Vargas,R., Nonogaki,H., Suslow,T. and Saltveit,M.
 TITLE Direct Submission
 JOURNAL Submitted (25-AUG-2000) Vegetable Crops, University of California
 Davis, One Shields Ave., Davis, CA 95616, USA
 COMMENT Method: conceptual translation supplied by author.
 FEATURES
 Location/Qualifiers
 source 1..711
 /organism="Lactuca sativa"
 /db_xref="taxon:4236"
 Protein 1..711
 /product="phenylalanine ammonia-lyase"
 /name="PAL1"
 CDS 1..711
 /coded_by="AF299330.1:119..2254"

ORIGIN

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1  mengnhvngv vnelcikdpl nwgvaeealt gshldevkkm vaefrkpvvk lggetltvsq
61  vagiaaands dtvkvelsea aragvkassd wvmesmknkg dsygvttgfg atshrtrkqg
121 galqkelirf lnagifngt etshtlphsa traamivrin tllqgysgir feileaitkf
181 lnnnitpcpl lrgtitasgd lvplsyiagl ltrpnskaav gptgevlvae kafaaagveg
241 gffelqpkeg lalvngtavg sgmasmvlfv anvlallsev lsaifaevmq gkpeftdhlt
301 hklkhpgqgi eaaameyil dgsdyvkaa qvhemdplqk pkqdryalrt spqwlqpgie
361 virsstkmie reinsvndnp lidvsrnkal hggnfqgtpi gvsmdntrla iaagiklmfa
421 qfselvndfy nnglpsnlsg grnpsldygf kggeiamasy cselqflanp vtnhvsaeq
481 hnqdvnsigl isarktaeav dilklmssty lvalcgsidl rhleenmkst vkntvsqvak
541 kvltmgvnge lhpsrfcekd llrvvdreyv fayiddvcsg typlmqklrq vlvdhalnng
601 etekntntsi fqkiatfeee lkvllpkeve gvriayendt lsipnrikac rsyplyrfvr
661 eelgrgfltg ekvtspgeef drvftamckg qiidpllecl ggwngeplpi c

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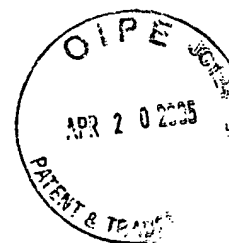
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Range: from to
 Features: ☐ SNP ☐ CDD ☒ MGC ☐ HPRD ☐ STS

☐ 1: [O49836](#). Reports Phenylalanine amm...[gi:3914262]

BLink, Domains,
Links

LOCUS O49836 705 aa linear PLN 01-MAY-2005
 DEFINITION Phenylalanine ammonia-lyase 2 (PAL-2).
 ACCESSION O49836
 VERSION O49836 GI:3914262
 DBSOURCE swissprot: locus PAL2_LITER, accession [O49836](#);
 class: standard.
 created: Dec 15, 1998.
 sequence updated: Dec 15, 1998.
 annotation updated: May 1, 2005.
 xrefs: [D83076.1](#), [BAA24929.1](#), [JC5873](#)
 xrefs (non-sequence databases): HSSPP21310, InterProIPR008948,
 InterProIPR001106, InterProIPR005922, PfamPF00221,
 TIGRFAMsTIGR01226, PROSITEPS00488
 KEYWORDS Lyase; Multigene family; Phenylpropanoid metabolism.
 SOURCE Lithospermum erythrorhizon
 ORGANISM Lithospermum erythrorhizon
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiids; Boraginaceae; Lithospermum.
 REFERENCE 1 (residues 1 to 705)
 AUTHORS Yazaki,K., Kataoka,M., Honda,G., Severin,K. and Heide,L.
 TITLE cDNA cloning and gene expression of phenylalanine ammonia-lyase in
 Lithospermum erythrorhizon
 JOURNAL Biosci. Biotechnol. Biochem. 61 (12), 1995-2003 (1997)
 PUBMED 9438980
 REMARK NUCLEOTIDE SEQUENCE.
 COMMENT On Apr 12, 2005 this sequence version replaced [gi:7437121](#).
 [FUNCTION] This is a key enzyme of plant metabolism catalyzing the
 first reaction in the biosynthesis from L-phenylalanine of a wide
 variety of natural products based on the phenylpropane skeleton.
 [CATALYTIC ACTIVITY] L-phenylalanine = trans-cinnamate + NH(3).
 [PATHWAY] Phenylpropanoid biosynthesis; first step.
 [SUBCELLULAR LOCATION] Cytoplasmic (Probable).
 [TISSUE SPECIFICITY] Expressed mainly in roots.
 [PTM] Contains an active site 4-methylidene-imidazole-5-one (MIO),
 which is formed autocatalytically by cyclization and dehydration of
 residues Ala-Ser-Gly (By similarity).
 [SIMILARITY] Belongs to the PAL/histidase family.
 FEATURES
 source Location/Qualifiers
 1..705
 /organism="Lithospermum erythrorhizon"
 /db_xref="taxon:[34254](#)"
 Protein 1..705
 /product="Phenylalanine ammonia-lyase 2"
 /EC_number="[4.3.1.5](#)"



Bond bond(191,193)
/bond_type="xlink"
/note="5-imidazolinone (Ala-Gly) (By similarity)."
/evidence=not_experimental
Site 192
/site_type="modified"
/note="2,3-didehydroalanine (Ser) (By similarity)."
/evidence=not_experimental



ORIGIN

```
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61  aarddgvtve  laeaaregvk  assdwvmesm  nkgtdsygvt  tgfgatshrr  tkqggalqke
121  lirflnagif  gngtetshtl  phsatraaml  vrintllggy  sgirfeilea  itkfltnnit
181  pclplrgtit  asgdlvplsy  iaglltgrpn  skavgptgek  lnaeeafrla  gissgffelq
241  pkeglalvng  tavsgmsasm  vlyeanilgv  msevlsavfa  evmngkpeft  dhlthklkhh
301  pgqieaaaam  ehildgsgyv  kaaellhemd  plqkpkqdry  alrtspqwlq  pqievirsat
361  kmiereinsv  ndnplidvsr  nkalhggnfq  gtpigvamd  trlaiaaigk  llfaqfselv
421  ndyynnglps  nltgsrdpsl  dygfkgaeia  masycselqf  lanpvtnhvq  saeqhnqdv  n
481  slglissrkt  seaveilkml  sssflvalcq  avdlrhieen  vrlavkktvs  qvakktlnig
541  vdgvlhpsrf  sekellrvvd  reyvfayadd  pcsatypmq  klrevlvsha  lansgnkda
601  stsifhkigv  feeelkgilp  kevenarasv  engtpaipnk  ieecrsyply  kfvrgegelte
661  lltgekvrs  geeldqvfn  lceglvdpl  lacleawnga  plpic
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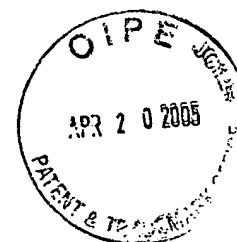
Limits Preview/Index History Clipboard Details

Range: from to Features: ☐ SNP ☐ CDD ☒ MGC ☐ HPRD ☐ STS

☐ 1: Q42858. Reports Phenylalanine amm...[gi:3024361]

[BLink](#), [Domains](#),
[Links](#)

LOCUS Q42858 708 aa linear PLN 01-MAY-2005
 DEFINITION Phenylalanine ammonia-lyase.
 ACCESSION Q42858
 VERSION Q42858 GI:3024361
 DBSOURCE swissprot: locus PAL2_IPOBA, accession Q42858;
 class: standard.
 created: Jul 15, 1998.
 sequence updated: Jul 15, 1998.
 annotation updated: May 1, 2005.
 xrefs: D78640.1, BAA11459.1, T10909
 xrefs (non-sequence databases): HSSPP21310, InterProIPR008948,
 InterProIPR001106, InterProIPR005922, PfamPF00221,
 TIGRFAMsTIGR01226, PROSITEPS00488
 KEYWORDS Lyase; Multigene family; Phenylpropanoid metabolism.
 SOURCE Ipomoea batatas (sweet potato)
 ORGANISM Ipomoea batatas
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiids; Solanales; Convolvulaceae; Ipomoeae; Ipomoea.
 REFERENCE 1 (residues 1 to 708)
 AUTHORS Tanaka, Y.
 TITLE Direct Submission
 JOURNAL Submitted (??-DEC-1995)
 REMARK NUCLEOTIDE SEQUENCE.
 STRAIN=cv. Beniazuma; TISSUE=Root
 COMMENT On Apr 12, 2005 this sequence version replaced gi:7437130.
 [FUNCTION] This is a key enzyme of plant metabolism catalyzing the
 first reaction in the biosynthesis from L-phenylalanine of a wide
 variety of natural products based on the phenylpropane skeleton.
 [CATALYTIC ACTIVITY] L-phenylalanine = trans-cinnamate + NH(3).
 [PATHWAY] Phenylpropanoid biosynthesis; first step.
 [SUBCELLULAR LOCATION] Cytoplasmic (Probable).
 [PTM] Contains an active site 4-methylidene-imidazole-5-one (MIO),
 which is formed autocatalytically by cyclization and dehydration of
 residues Ala-Ser-Gly (By similarity).
 [SIMILARITY] Belongs to the PAL/histidase family.
 FEATURES
 source Location/Qualifiers
 1..708
 /organism="Ipomoea batatas"
 /db_xref="taxon:4120"
 Protein 1..708
 /product="Phenylalanine ammonia-lyase"
 /EC_number="4.3.1.5"
 Bond bond(194,196)
 /bond_type="xlink"



Site

/note="5-imidazolinone (Ala-Gly) (By similarity)."
 /evidence=not_experimental
 195
 /site_type="modified"
 /note="2,3-didehydroalanine (Ser) (By similarity)."
 /evidence=not_experimental

ORIGIN



```

1 megaianght ndfcikvdpl nwemaadslk gshldevkrm vaefrnpavk iggqtltslr
61 sppiaardna skwssprlpa rresssdwvm nsmnngtdsy gvttgfgats hrrtknghal
121 qqelirflna gifgtgtgas htlphsatra amlvrintl1 qgysgirfei leaitkllnh
181 nitpclplrg titasgdlvp lsyiaglltg rpnskavgpn gealtaeeaf klagvqggff
241 elqpkeglal vngtavsgsm asmvlfearv lavlsevlsa ifaevmngkp eftdhlthkl
301 khhpqgieaa aimehildrs yymkaaqlh emdplqkpkq dryalrtspq wlgppqievir
361 qatkmierei nsvndnplid vsrnkalhgg nfggtpigvs mdnsrlalas igklifaqfs
421 elvndyynnng lpsnltagrn psldygfkqv eiamasycse lqflanpvtn hvqsaeqhnq
481 dvnsllglisa rktaeavdvl klmsstylva lcqaidlrhl eenlknavrnt tvnqvakrtl
541 tmgvngelhp srfcekdllr vvdreyvfay addpcsanyp lfqklrqvlv dhalqngehe
601 knvstsifqk iaafedelka vlpkevegar saiengnpai pnritecrsy plykfvreel
661 gtemltgekv kspgevcdkv ftavcdggii dplleclksw dgaplpic
    
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Range: from to
 Features:
 ☐ SNP
 ☐ CDD
 ☒ MGC
 ☐ HPRD
 ☐ STS

☐ 1: [P19142](#). Reports Phenylalanine amm...[gi:129585]

[BLink](#), [Domains](#),
[Links](#)

LOCUS P19142 712 aa linear PLN 01-MAY-2005
 DEFINITION Phenylalanine ammonia-lyase class II.
 ACCESSION P19142
 VERSION P19142 GI:129585
 DBSOURCE swissprot: locus PAL2_PHAVU, accession [P19142](#);
 class: standard.

created: Nov 1, 1990.
 sequence updated: Nov 1, 1990.
 annotation updated: May 1, 2005.
 xrefs: [S04127](#)

xrefs (non-sequence databases): [HSSPP21310](#), [InterProIPR008948](#),
[InterProIPR001106](#), [InterProIPR005922](#), [PfamPF00221](#),
[TIGRFAMsTIGR01226](#), [PROSITEPS00488](#)

KEYWORDS Lyase; Multigene family; Phenylpropanoid metabolism.

SOURCE *Phaseolus vulgaris*

ORGANISM *Phaseolus vulgaris*

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Phaseolus.

REFERENCE 1 (residues 1 to 712)

AUTHORS Cramer,C.L., Edwards,K., Dron,M., Liang,X., Dildine,S.L.,
 Bolwell,G.P., Dixon,R.A., Lamb,C.J. and Schuch,W.

TITLE Phenylalanine ammonia-lyase gene organisation and structure

JOURNAL Plant Mol. Biol. 12, 367-383 (1989)

REMARK NUCLEOTIDE SEQUENCE.

COMMENT On Apr 12, 2005 this sequence version replaced [gi:81877](#).

[FUNCTION] This is a key enzyme of plant metabolism catalyzing the
 first reaction in the biosynthesis from L-phenylalanine of a wide
 variety of natural products based on the phenylpropane skeleton.

[CATALYTIC ACTIVITY] L-phenylalanine = trans-cinnamate + NH(3).

[PATHWAY] Phenylpropanoid biosynthesis; first step.

[SUBCELLULAR LOCATION] Cytoplasmic (Probable).

[PTM] Contains an active site 4-methylidene-imidazole-5-one (MIO),
 which is formed autocatalytically by cyclization and dehydration of
 residues Ala-Ser-Gly (By similarity).

[SIMILARITY] Belongs to the PAL/histidase family.

FEATURES Location/Qualifiers

source 1..712

/organism="Phaseolus vulgaris"

/db_xref="taxon:3885"

Protein 1..712

/product="Phenylalanine ammonia-lyase class II"

/EC_number="4.3.1.5"

Bond bond(198,200)

Site

/bond_type="xlink"
/note="5-imidazolinone (Ala-Gly) (By similarity)."
/evidence=not_experimental
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/note="2,3-didehydroalanine (Ser) (By similarity)."
/evidence=not_experimental

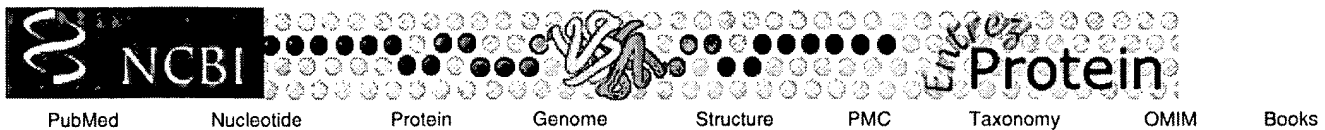
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121 ggalqkelir flnagifgng tesnctlpht atraamlvrp ntllqgyysi rfeileaitk  
181 llnnnitpcl plrgtitasg dlvpalsyia lltgrpnksa vgpsgeilna keafelanig  
241 seffelpke glalvngtav gsglasivlf eanilavlse visaifaevm qgkpeftdhl  
301 thklkhpgq ieaaaimehi ldgssyikaa kklheidplq kpkqdryalr tspqwlpgqi  
361 evirfstksi ereinsvndn plisvsrnka lhggmfqgtp igvsmndntrl aiasigklmf  
421 aqfsdlvndy ynnglpsnlt asrnpsldyg fkgaeiamas ycselqylan pvtshvqsae  
481 qhnqdvnslg lissrktnea leilkmsst flvalcqaid lrhleenlkn tvknvvsqva  
541 krtlttgvg elhpsrfcek allkvverey tfayiddpcs gtyplmqklr qvlvdyalan  
601 geneknlnts ifqkiasfee elktllpkev egarlayend qcaipnkikd crsyplykfv  
661 reelgtsllt gekvispgee cdkvfsamcq gkiidpllec lgewngaplp ic
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Range: from to Features: ☐ SNP ☐ CDD ☒ MGC ☐ HPRD ☐ STS

☐ 1: [CAA57057](#). Reports phenylalanine amm...[gi:535008]

BLink, Domains,
Links

LOCUS CAA57057 718 aa linear PLN 07-DEC-1994
 DEFINITION phenylalanine ammonia-lyase 3 [Petroselinum crispum].
 ACCESSION CAA57057
 VERSION CAA57057.1 GI:535008
 DBSOURCE embl locus PCPAL3, accession [X81159.1](#)
 KEYWORDS .
 SOURCE Petroselinum crispum (parsley)
 ORGANISM Petroselinum crispum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; campanulids; Apiales; Apiaceae; Apioideae; apioid
 superclade; Apium clade; Petroselinum.
 REFERENCE 1
 AUTHORS Appert,C., Logemann,E., Hahlbrock,K., Schmid,J. and Amrhein,N.
 TITLE Structural and catalytic properties of the four phenylalanine
 ammonia-lyase isoenzymes from parsley (Petroselinum crispum Nym.)
 JOURNAL Eur. J. Biochem. 225 (1), 491-499 (1994)
 PUBMED [7925471](#)
 REFERENCE 2 (residues 1 to 718)
 AUTHORS Appert,C.
 TITLE Direct Submission
 JOURNAL Submitted (22-AUG-1994) C. Appert, Institut fuer
 Pflanzenwissenschaften, Eidgenoessische Technische Hochschule,
 Zuerich, Universitaetsstrasse 2, 8092 Zurich, SWITZERLAND
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 /organism="Petroselinum crispum"
 /db_xref="taxon:4043"
 Protein 1..718
 /product="phenylalanine ammonia-lyase 3"
 /EC_number="4.3.1.5"
 CDS 1..718
 /gene="PAL3"
 /coded_by="X81159.1:89..2245"
 /note="tetramere subunit"
 /db_xref="GOA:P45729"
 /db_xref="UniProt/Swiss-Prot:P45729"

ORIGIN

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1 mayvngttnng hangngldlc mkkedplnwg vaaealtgsh ldevkrmvae yrkpvvkleg
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121 rrtkqggalq kelirflnag ifgsgaeagn ntlphsatra amlvrintll qgysgirfei
181 leaitkflnh nitpclplrg titasgdlvp lsyiaglltg rpnskavgpt gvtlspeeaf
241 klagveggff elqpkeglal vngtavsgsm asmvlfeari lavlaevmsa ifaevmqqkp
301 eftdhltkl khhpgqieaa aimehildgs ayvkaaqlh emdplqkpkq dryalrtspq
361 wlqpqievir sstkmierei nsvndnplid vsrnkaihgg nfqgspigvs mdntrlaiaa



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421 igklmfaqfs elvndfynng lpsnlsggrn psldygfkga eiamasycse lqflanpvtn
481 hvgsaeqhnq dvnslgliiss rktseaveil klmsttflvg lcqaidlrhl eenlkstvkn
541 tvsqvakrvl tmgvngelhp srfcekdllr vvdreyifay iddpccsatyp lmqklretlv
601 ehalnngdke rnlstsifqk iaafedelka llpkevetar aalesgnpai pnrikecrsy
661 plykfvreel gteyltgekv rspgeefekv ftamskgeii dplleclesw ngaplpic

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Range: from to Features: ☐ SNP ☐ CDD ☒ MGC ☐ HPRD ☐ STS

☐ 1: [AAF40224](#). Reports phenylalanine amm...[gi:7208616]

BLink, Domains,
Links

LOCUS AAF40224 730 aa linear PLN 19-SEP-2001
 DEFINITION phenylalanine ammonia-lyase 2 [Rubus idaeus].
 ACCESSION AAF40224
 VERSION AAF40224.1 GI:7208616
 DBSOURCE locus AF237955 accession [AF237955.1](#)
 KEYWORDS
 SOURCE Rubus idaeus
 ORGANISM Rubus idaeus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Rubus.
 REFERENCE 1 (residues 1 to 730)
 AUTHORS Kumar,A. and Ellis,B.E.
 TITLE The phenylalanine ammonia-lyase gene family in raspberry.
 Structure, expression, and evolution
 JOURNAL Plant Physiol. 127 (1), 230-239 (2001)
 PUBMED [11553751](#)
 REFERENCE 2 (residues 1 to 730)
 AUTHORS Kumar,A. and Ellis,B.E.
 TITLE Direct Submission
 JOURNAL Submitted (23-FEB-2000) The Biotechnology Laboratory and Faculty of
 Agricultural Sciences, University of British Columbia, 344-2357
 Main Mall, Vancouver, BC V6T 1Z4, Canada
 COMMENT Method: conceptual translation supplied by author.
 FEATURES
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 /organism="Rubus idaeus"
 /db_xref="taxon:32247"
 /dev_stage="fruit"
 Protein 1..730
 /product="phenylalanine ammonia-lyase 2"
 /EC_number="4.3.1.5"
 /name="PAL; phenylpropanoid; multigene; flavonoid"
 CDS 1..730
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 /coded_by="AF237955.1:66..2258"

ORIGIN

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121 sygvttgfga tshrtrkqga alqkelirfl nagvlrngte sahtlphsat raamlvrnt
181 llqgysgirf eileaiskfl nhnitpcplpl rgtitasgdl vplsyaigll tgrpnskavg
241 pkgetlnaae afaqvgissg ffelqpkegl alvngtavgs glastvlfet nilallseil
301 saifaevmqg kpeftdhlth klkhhpggie aaaimehild gssyvkaaek lheqdpqlkp
361 kqdryalrts pqwlgpgiev irfstksier einsvndnpl idvsrnkalh ggnfqgtpig
421 vsmdntrlai asigklmfaq fselvndfyn nglpsnlsdg rdpsldygfk gaeiamasye



```

481 selqflanpv tnhvgsaeqh nqdvnsigli ssrktaeavd ilkmsstfl valcqaidlr
541 hleenlkstv kntvsqakr vlttgvgel hpsrfcekd lmvvereylf ayiddpcsat
601 yplmqrlrqv lvehaltng neknastsif qkitafeeel ktilpkeves araayesgna
661 aipnrivecr syplykfvre elggeflte kvrspgeecd kvftamcqqn iidpildcls
721 gwngelpic

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PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

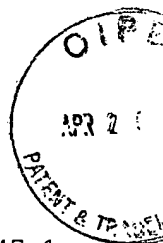
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Range: from to
 Features: ☐ SNP ☐ CDD ☒ MGC ☐ HPRD ☐ STS

☐ 1: P35510. Reports Phenylalanine amm...[gi:1171991]
 BLink, Domains, Links

LOCUS P35510 725 aa linear PLN 01-MAY-2005
 DEFINITION Phenylalanine ammonia-lyase 1.
 ACCESSION P35510
 VERSION P35510 GI:1171991
 DBSOURCE swissprot: locus PAL1_ARATH, accession P35510;
 class: standard.
 extra accessions: Q9ZQD6, created: Jun 1, 1994.
 sequence updated: Nov 1, 1995.
 annotation updated: May 1, 2005.
 xrefs: L33677.1, AAC18870.1, AC006922.7, AAM15324.1, X62747.1,
CAA44609.1, S52990
 xrefs (non-sequence databases): HSSPP21310, InterProIPR008948,
 InterProIPR001106, InterProIPR005922, PfamPF00221,
 TIGRFAMsTIGR01226, PROSITEPS00488
 KEYWORDS Lyase; Multigene family; Phenylpropanoid metabolism.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (residues 1 to 725)
 AUTHORS Wanner, L.A., Li, G., Ware, D., Somssich, I.E. and Davis, K.R.
 TITLE The phenylalanine ammonia-lyase gene family in Arabidopsis thaliana
 JOURNAL Plant Mol. Biol. 27 (2), 327-338 (1995)
 PUBMED 7888622
 REMARK NUCLEOTIDE SEQUENCE.
 STRAIN=cv. Landsberg erecta
 REFERENCE 2 (residues 1 to 725)
 AUTHORS Lin, X., Kaul, S., Rounsley, S., Shea, T.P., Benito, M.I., Town, C.D.,
 Fujii, C.Y., Mason, T., Bowman, C.L., Barnstead, M., Feldblyum, T.V.,
 Buell, C.R., Ketchum, K.A., Lee, J., Ronning, C.M., Koo, H.L.,
 Moffat, K.S., Cronin, L.A., Shen, M., Pai, G., Van Aken, S., Umayam, L.,
 Tallon, L.J., Gill, J.E., Adams, M.D., Carrera, A.J., Creasy, T.H.,
 Goodman, H.M., Somerville, C.R., Copenhaver, G.P., Preuss, D.,
 Nierman, W.C., White, O., Eisen, J.A., Salzberg, S.L., Fraser, C.M. and
 Venter, J.C.
 TITLE Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana
 JOURNAL Nature 402 (6763), 761-768 (1999)
 PUBMED 10617197
 REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 STRAIN=cv. Columbia
 REFERENCE 3 (residues 1 to 725)
 AUTHORS Ohl, S., Hedrick, S.A., Chory, J. and Lamb, C.J.
 TITLE Functional properties of a phenylalanine ammonia-lyase promoter



from Arabidopsis
JOURNAL Plant Cell 2 (9), 837-848 (1990)
PUBMED 2152131
REMARK NUCLEOTIDE SEQUENCE OF 1-240.
STRAIN=cv. Columbia
COMMENT On or before Apr 12, 2005 this sequence version replaced
gi:1076369, gi:548456.
[FUNCTION] This is a key enzyme of plant metabolism catalyzing the
first reaction in the biosynthesis from L-phenylalanine of a wide
variety of natural products based on the phenylpropane skeleton.
[CATALYTIC ACTIVITY] L-phenylalanine = trans-cinnamate + NH(3).
[PATHWAY] Phenylpropanoid biosynthesis; first step.
[SUBCELLULAR LOCATION] Cytoplasmic (Probable).
[PTM] Contains an active site 4-methylidene-imidazole-5-one (MIO),
which is formed autocatalytically by cyclization and dehydration of
residues Ala-Ser-Gly (By similarity).
[SIMILARITY] Belongs to the PAL/histidase family.

FEATURES

Location/Qualifiers

source 1..725
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"

gene 1..725
/gene="PAL1"
/locus_tag="At2g37040"
/note="synonym: T1J8.22"

Protein 1..725
/gene="PAL1"
/locus_tag="At2g37040"
/product="Phenylalanine ammonia-lyase 1"
/EC_number="4.3.1.5"

Bond bond(211,213)
/gene="PAL1"
/locus_tag="At2g37040"
/bond_type="xlink"
/note="5-imidazolinone (Ala-Gly) (By similarity)."
/evidence=not_experimental

Site 212
/gene="PAL1"
/locus_tag="At2g37040"
/site_type="modified"
/note="2,3-didehydroalanine (Ser) (By similarity)."
/evidence=not_experimental

Region 329
/gene="PAL1"
/locus_tag="At2g37040"
/region_name="Conflict"
/note="V -> I (in Ref. 2)."
/evidence=experimental

Region 426
/gene="PAL1"
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/region_name="Conflict"
/note="R -> A (in Ref. 2)."
/evidence=experimental

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/note="V -> I (in Ref. 2)."
/evidence=experimental

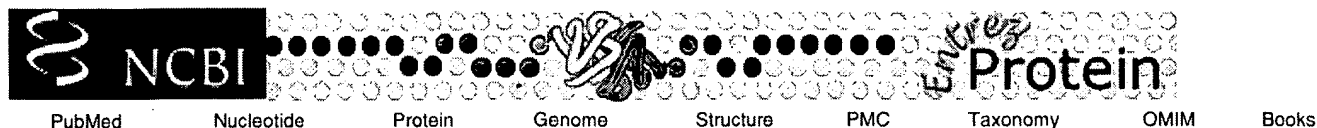
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181 sgirfeilea itsflnnnit pslplrgrtit asgdlvpls iaglltgrpn skatgpngea
241 ltaeeafkla gissgffdlq pkeglalvng tavgsgmasm vlfetnvlsv laeilsavfa
301 evmsgkpeft dhlthrlkhh pgqieaaaavm ehildgssym klaqklhemd plqkpkqdry
361 alrtspqwlq pqieviryat ksiereinsv ndnplidvsr nkaihggnfq gtpigvsmdn
421 trlairaigk lmfaqfselv ndfynnglps nltasrnpsl dygfkgaeia masycselqy
481 lanpvtshvq saeqhnqdv nslglissrkt seavdilklm sttflvaicq avdlrhleen
541 lrqtvkntvs qvakkvlttg vngelhpsrf cekdllkvvd reqvytyadd pcsatypli
601 klrqvivdha lvngesekna vtsifhkiga feeelkavlp keveaaraay dngtsaipnr
661 ikecrsyply rfvreelgte lltgekvts pgefdkvfta icegkiidpm meclnewnga
721 pipic
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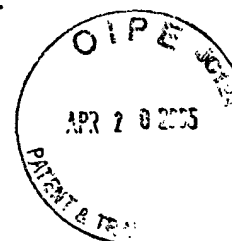
☒ ☒

Range: from to Features: ☐ SNP ☐ CDD ☒ MGC ☐ HPRD ☐ STS

☐ 1: [CAA35886](#). Reports phenylalanine amm...[gi:3294]

BLink, Domains,
Links

LOCUS CAA35886 716 aa linear PLN 28-NOV-1996
 DEFINITION phenylalanine ammonia-lyase [Rhodosporidium toruloides].
 ACCESSION CAA35886
 VERSION CAA35886.1 GI:3294
 DBSOURCE embl locus RTPAL2, accession [X51513.1](#)
 KEYWORDS .
 SOURCE Rhodosporidium toruloides
 ORGANISM [Rhodosporidium toruloides](#)
 Eukaryota; Fungi; Basidiomycota; Urediniomycetes;
 Microbotryomycetidae; Sporidiobolales; Rhodosporidium.
 REFERENCE 1 (residues 1 to 716)
 AUTHORS Rasmussen, O.F. and Oerum, H.
 TITLE Analysis of the gene for phenylalanine ammonia-lyase from
 Rhodosporidium toruloides
 JOURNAL DNA Seq. 1 (3), 207-211 (1991)
 PUBMED [1773059](#)
 REFERENCE 2 (residues 1 to 716)
 AUTHORS Petersen, S.K.
 TITLE Direct Submission
 JOURNAL Submitted (23-JAN-1990) Petersen S.K., Genetic Engineering Group,
 Technical University of Denmark, Building 227, DK 2800 Lyngby,
 Denmark
 COMMENT See also <M18261> for R.toruloides strain IFO 0559 pal gene.
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 source 1..716
 /organism="Rhodosporidium toruloides"
 /strain="CBS 14"
 /db_xref="taxon:5286"
 /clone_lib="Centraalbureau voor Schimmelcultures"
 Protein 1..716
 /product="phenylalanine ammonia-lyase"
 CDS 1..716
 /gene="pal"
 /coded_by="join(X51513.1:519..829,X51513.1:919..1005,
 X51513.1:1067..1201,X51513.1:1259..1835,
 X51513.1:1897..2063,X51513.1:2123..2411,
 X51513.1:2468..3052)"
 /db_xref="GOA:P11544"
 /db_xref="UniProt/Swiss-Prot:P11544"
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 121 dtrtedaisl qkallehqlc gvlpsfsdf rlgrglensl plevvrgamt irvnsltrgh
 181 savrlvlea ltnflnhgit pivplrgtis asgdlsplsy iaaaishghpd skvhvvhgk
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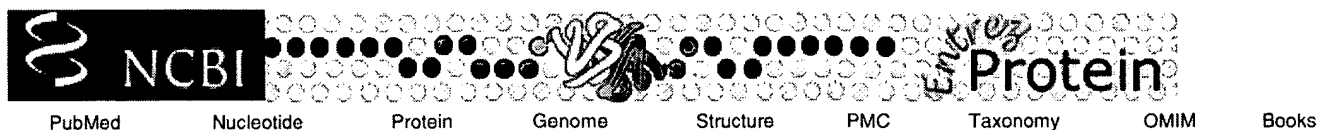



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421 tmektrlgla qigklnftql temlnagmnr glpsclaaed pslyhckgl diaaaaytse
481 lghlanpvtv hvqpaemang avnslalisa rrttesndvl slllathlyc vlqaidlrai
541 efefkkqfgp aivslidqhf gsamtgsnlr delvekvnt lakrleqtms ydlvprwhda
601 fsfaagtvve vlsstslsla avnawkvaas esaisltrqv retfwsaast sspalsylsp
661 rtqilyafvr eelgvkarrg dvflgkqevt igsnvskiye aiksgrinna llkmla
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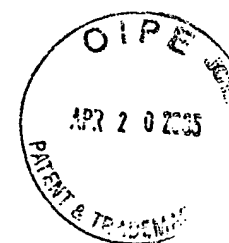
Limits Preview/Index History Clipboard Details

Range: from to Features: ☐ SNP ☐ CDD ☒ MGC ☐ HPRD ☐ STS

☐ 1: [AAA33883](#). Reports phenylalanine amm...[gi:169746]

[BLink](#), [Domains](#),
[Links](#)

LOCUS AAA33883 693 aa linear PLN 27-APR-1993
 DEFINITION phenylalanine ammonia-lyase.
 ACCESSION AAA33883
 VERSION AAA33883.1 GI:169746
 DBSOURCE locus RHPAL accession [M18261.1](#)
 KEYWORDS .
 SOURCE Rhodosporidium toruloides
 ORGANISM [Rhodosporidium toruloides](#)
 Eukaryota; Fungi; Basidiomycota; Urediniomycetes;
 Microbotryomycetidae; Sporidiobolales; Rhodosporidium.
 REFERENCE 1 (residues 1 to 693)
 AUTHORS Anson,J.G., Gilbert,H.J., Oram,J.D. and Minton,N.P.
 TITLE Complete nucleotide sequence of the Rhodosporidium toruloides gene
 coding for phenylalanine ammonia-lyase
 JOURNAL Gene 58 (2-3), 189-199 (1987)
 PUBMED [2828184](#)
 COMMENT Method: conceptual translation.
 FEATURES Location/Qualifiers
 source 1..693
 /organism="Rhodosporidium toruloides"
 /db_xref="taxon:5286"
 Protein 1..693
 /name="phenylalanine ammonia-lyase"
 CDS 1..693
 /coded_by="join(M18261.1:354..595,M18261.1:687..773,
 M18261.1:835..969,M18261.1:1027..1603,M18261.1:1665..1831,
 M18261.1:1891..2179,M18261.1:2236..2820)"



ORIGIN

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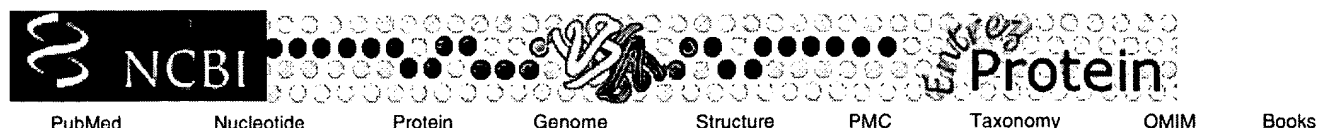
1 maprptsqsg artcpttqvt qvdivekmla aptdstleld gyslnlgdvv saarkgrpvr
61 vkdsdeirsk idksveflrs qlmsvygvt tgfggsadtr tedaislqka llehqlcgv
121 pssfdsfrlg rglenslple vvirgamtirv nsltrghsav rlvvlealt n flnhgitpiv
181 plrgtisasg dlsplsyiaa aisghpdskv hvvhgkeki lyareamalf nlepvvlgpk
241 eglglvngta vsasmatlal hdahmlslls qsltamvea mvghagsfhp flhdvtrph
301 tqievagnir kllegsrfav hheeevkvkd degilrqdry plrtspqwl p lvsdliha
361 avltieagqs ttdnplidve nktshhggnf gaaavantme ktrlglaqig klnftqlte
421 lnagmnr glp sclaaedpsl syhckgldia aaaytselgh lanpvtthvq paemanqav
481 slalisarrt tesndvlsll lathlycvlq aidlraiefe fkkqfgpaiv slidqhfgsa
541 mtgsnlrdel vekvnktlak rleqtnsydl vprwhdafsf aagt vvevls stslslaavn
601 awkvaasesa isltrqvret fwsaastssp alsylsprtq ilyafvree l gvkarrgdvf
661 lgkqevtigs nvskiyeaik sgrinnvllk mla

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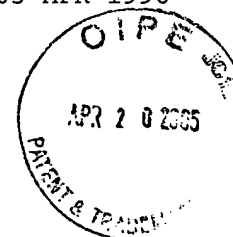
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 Range: from to Features: ☐ SNP ☐ CDD ☒ MGC ☐ HPRD ☐ STS☐ 1: [1314202A](#). Reports Phe ammonia lyase...[gi:225818]BLink, Domains,
Links

LOCUS 1314202A 705 aa linear PLN 05-APR-1996
DEFINITION Phe ammonia lyase.
ACCESSION 1314202A
VERSION 1314202A GI:225818
DBSOURCE prf: locus 1314202A;

state: glioblastoma derived T cell;
taxonomy: Fungi.KEYWORDS Phe Ammonia Lyase; pal Gene; Rhodosporidium toruloides;
cDNA/Genomic Clone; Seq Determination; 2980bp; 582AAs; Exon x7; Seq
Comparison; Codon Usage.

SOURCE Rhodosporidium toruloides

ORGANISM Rhodosporidium toruloidesEukaryota; Fungi; Basidiomycota; Urediniomycetes;
Microbotryomycetidae; Sporidiobolales; Rhodosporidium.

REFERENCE 1 (residues 1 to 705)

AUTHORS Anson, J.G., Gilbert, H.J., Oram, J.D. and Minton, N.P.

TITLE Complete nucleotide sequence of the Rhodosporidium toruloides gene
coding for phenylalanine ammonia-lyase

JOURNAL Gene 58(2/3), 189-199 (1987)

COMMENT gene.pal exon.x7.

FEATURES Location/Qualifiers

source 1..705

/organism="Rhodosporidium toruloides"

/db_xref="taxon:5286"



ORIGIN

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61 vkdsdeirsk idksveflrs qlsmsvygvt tgfggsadtr tedaislqka llehqdaisl
121 qkalcgvlpv sfdsfrlgrg lenslplevv rgamtirvns ltrghsavrl vvlealtnfl
181 nhgitpivpl rgtisasgdl splsyiaaaai sgphdskvhv vhegkekily areamalfnl
241 epvvlgpkeg lglvngtavs asmatlalhda ahmlslslsq ltamtveamv ghagsfhpfl
301 hdvtrphptq ievagnirk1 legsrfavhh eeevkvkdde gilrqdrypl rtspqwlgpl
361 vsdlihahav ltieaggstt dnplidvenk tshhggnfqa aavantmekt rlglagigkl
421 nftqltemln agmnrplpsc laaedpslsy hckgldiaaa aytselghll nftanpvttth
481 vqpaemanga vnslalisar rttesndvls lllathlycv lqaidlraie fefkkqfgpa
541 ivslidqhfg samtgsnlrd elvekvntkl akrleqtnsy dlvrwhdaf sfaagtvvvev
601 lsstslslaa vnawkvaaae saisltrqvr etfwsaasts spalsylspr tqilyafvre
661 elgvkarrgd vflgkqevti gsnvskiyea iksgrinnvl lkmla
```

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Range: from to
 Features:
 ☐ SNP
 ☐ CDD
 ☒ MGC
 ☐ HPRD
 ☐ STS

☐ 1: CAA31486. Reports phenylalanine amm...[gi:295942]

BLink, Domains,
Links

LOCUS CAA31486 713 aa linear PLN 30-MAR-1999
 DEFINITION phenylalanine ammonia-lyase [Rhodotorula mucilaginosa].
 ACCESSION CAA31486
 VERSION CAA31486.1 GI:295942
 DBSOURCE embl locus RRPAL, accession [X13094.1](#)
 KEYWORDS .
 SOURCE Rhodotorula mucilaginosa
 ORGANISM [Rhodotorula mucilaginosa](#)
 Eukaryota; Fungi; Basidiomycota; Urediniomycetes;
 Microbotryomycetidae; Sporidiobolales; mitosporic Sporidiobolales;
 Rhodotorula.

REFERENCE 1
 AUTHORS Filpula,D., Vaslet,C.A., Levy,A., Sykes,A. and Strausberg,R.L.
 TITLE Nucleotide sequence of gene for phenylalanine ammonia-lyase from
 Rhodotorula rubra
 JOURNAL Nucleic Acids Res. 16 (23), 11381 (1988)
 PUBMED [3205749](#)

REFERENCE 2 (residues 1 to 713)
 AUTHORS Filpula,D.
 TITLE Direct Submission
 JOURNAL Submitted (28-SEP-1988) Filpula D., Genex Corporation, 16020
 Industrial Drive, Gaithersburg, MD 20877, USA

FEATURES Location/Qualifiers
 source 1..713
 /organism="Rhodotorula mucilaginosa"
 /strain="NRRLY-15597"
 /db_xref="taxon:5537"
 Protein 1..713
 /product="phenylalanine ammonia-lyase"
 CDS 1..713
 /gene="PAL"
 /coded_by="join(X13094.1:646..974,X13094.1:1062..1148,
 X13094.1:1231..1930,X13094.1:2011..2177,
 X13094.1:2247..2409,X13094.1:2484..3179)"
 /db_xref="GOA:P10248"
 /db_xref="UniProt/Swiss-Prot:P10248"

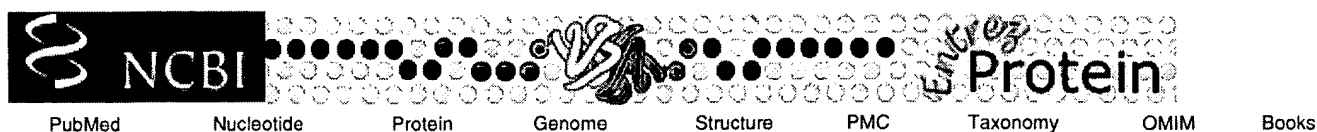
ORIGIN
 1 mapsvdsiat svanslsngl haaaaanggd vhkktagags llpttettql diverilada
 61 gatdqikldg ytltlgdvvg aarrgrsvkv adsphireki dasveflrtq ldnsvygvtt
 121 gfggsadtrt edaislqkal lehqlcgvlp tsmdgfalgr glenslplev vrgamtirvn
 181 sltrghsavr ivvlealtnf lnhgitpivp lrgtisagds lsplsyaas itghpdskvh
 241 vdgkimsaqe aialkgqlqv vlgpkeglvl vngtavsasm atlaltdahv lsllaqalta
 301 ltveamvgha gsfhpfldhv trphptgiev anirtlleg skyavhhete vkvkddgil
 361 rqdryplrsc pqwlgplvsd mihahavlsl eaggsttdnp lidlenkmth hggafmassv
 421 gntmektrla valmgkvsft qltemlnagm nralpsclaa edpslsyhck gldiaaaayt

481 selghlanpv sthvgpaemg ngainslali sarrtaeand vlsillathl ycvlgavdlr
541 amefehtkaf epmvteilkq hfgalataev edkvrksiyk rlqgnnsydl egrwhdtfsv
601 atgavveala ggevslasln awkvacaeka ialtrsvrds fwaapssssp alkylsprtr
661 vlysfvreev gvkarrgdvy lgkqevtigt nvsriyeaik sgciapvlvk mma

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☐ 1: [CAA09013](#). Reports phenylalanine amm...[gi:4127289]

[BLink](#), [Domains](#),
[Links](#)

LOCUS CAA09013 740 aa linear PLN 15-APR-2005
 DEFINITION phenylalanine ammonium lyase [*Amanita muscaria*].
 ACCESSION CAA09013
 VERSION CAA09013.1 GI:4127289
 DBSOURCE embl locus AAJ10143, accession [AJ010143.1](#)
 KEYWORDS .
 SOURCE *Amanita muscaria* (fly agaric)
 ORGANISM *Amanita muscaria*

Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;

Agaricales; Amanitaceae; Amanita.

REFERENCE 1
 AUTHORS Nehls,U., Ecke,M. and Hampp,R.
 TITLE Sugar- and nitrogen-dependent regulation of an *Amanita muscaria* phenylalanine ammonium lyase gene
 JOURNAL J. Bacteriol. 181 (6), 1931-1933 (1999)
 PUBMED [10074091](#)

REFERENCE 2 (residues 1 to 740)
 AUTHORS Nehls,U.
 TITLE Direct Submission
 JOURNAL Submitted (05-AUG-1998) Nehls U., Universitaet Tuebingen, Botanisches Institut, Physiologische Oekologie der Pflanzen, Auf der Morgenstelle 1, Tuebingen 72076, GERMANY

FEATURES
 source 1..740
 /organism="Amanita muscaria"
 /db_xref="taxon:41956"
 Protein 1..740
 /product="phenylalanine ammonium lyase"
 CDS 1..740
 /gene="PAL"
 /coded_by="AJ010143.1:18..2240"
 /db_xref="GOA:O93967"
 /db_xref="InterPro:IPR001106"
 /db_xref="InterPro:IPR005922"
 /db_xref="InterPro:IPR008948"
 /db_xref="UniProt/Swiss-Prot:O93967"

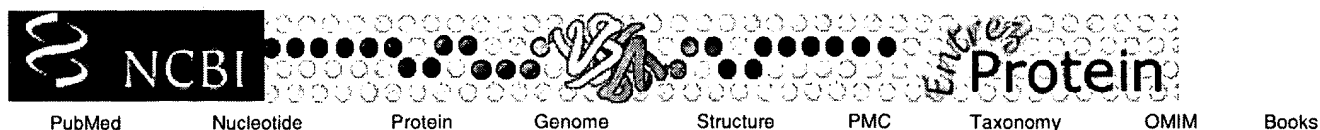
ORIGIN
 1 mgldnsknta kffdlpkavh gmngttpvng fkatalskas rtmktksals qfleayrele
 61 gykngraiqv dgqtlisiaav aaarynaav eldesplvke rvrksqlaia nkvstgasvy
 121 glstgfggsa dtrtdkpmll gfallqhqv gilptstapl dvlplqdan tsmpeawirg
 181 ailirmsli rghsgirwel iekmrellaa nvipvvplrg siassgdlspl lsyiahtiig
 241 npsikvyhgp sksgirqigs skdvlalhni epfpleskep lgilngtafs asvaalalne
 301 aihlvllaqv ctamgteali gtrashapfi hatarphpgq vecaeniwnl ldgsklaqle
 361 ehevrleddk ytlrqdrypl rtspqflgpq iediisafqt vtqecnylpa tdnplidget
 421 geshhggnfq amavtnamek trlalhvhgk llfsqstelv npamnrglpp svaatdpsln


```
481 yhakgldiat aayvaeatpg pthiqsaemh ngavnsllali saratitsle vltsliasyl
541 yilcgalldr alqreflpgl diiireelrs sfgsflsseq meklqqnlts afedhldktt
601 tmdntdrmtt maatsssvll qfftdsgasv ppsscdllss vssfqssvat rssvlmddlr
661 keyifgdrgp tpaqyigkt rpvqfirtt igvrkhgsen ynkfynglgv edvtigqnis
721 riyesirdgk mqsiiivslfd
```

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Range: from **begin** to **end** Features: ☐ SNP ☐ CDD ☒ MGC ☐ HPRD ☐ STS

☐ **1: AAC18871. Reports phenylalanine amm...[gi:497421]**

BLink, Domains,
Links

LOCUS AAC18871 717 aa linear PLN 04-JUN-1998
 DEFINITION phenylalanine ammonia lyase [Arabidopsis thaliana].
 ACCESSION AAC18871
 VERSION AAC18871.1 GI:497421
 DBSOURCE locus ATHPAL2 accession [L33678.1](#)
 KEYWORDS .
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM [Arabidopsis thaliana](#)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (residues 1 to 717)
 AUTHORS Wanner,L.A., Li,G., Ware,D., Somssich,I.E. and Davis,K.R.
 TITLE The phenylalanine ammonia-lyase gene family in Arabidopsis thaliana
 JOURNAL Plant Mol. Biol. 27 (2), 327-338 (1995)
 PUBMED [7888622](#)
 COMMENT Method: conceptual translation.

FEATURES Location/Qualifiers
 source 1..717
 /organism="Arabidopsis thaliana"
 /strain="Columbia"
 /db_xref="taxon:3702"
 /tissue_lib="MboI partial digestion in lambda EMBL4"
 Protein 1..717
 /product="phenylalanine ammonia lyase"
 /EC_number="4.3.1.5"
 CDS 1..717
 /gene="PAL2"
 /coded_by="join(L33678.1:1466..1869,L33678.1:2080..3829)"

ORIGIN

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1 mdqieamlcg ggektkvavt tktladplnw glaadqmkgs hldevkkmve eyrrpvvnlg
61 getltigqva aistvggsvk velaetsrag vkassdwvme smnkgtdsyg vttgfgatsh
121 rrtkngtalq telirflnag ifgntketch tlpqsatraa mlvrvtllq gysgirfeil
181 eaitsllnhn ispslplrgt itasghlvpl syiaglltgr pnskatgpdg esltekeafe
241 kagistgffd lqpkeglalv ngtagvsgma smvlfeanvq avlaevlsai faevmsgkpe
301 ftdhlthrlk hhpqqieaaa imehildgss ymklaqkvhe mdplqkpkqd ryalrtspqw
361 lgpqievirg atksierein svndnplidv srnkaihggg fggtpigvsm dntrlaiaai
421 gklmfaqfse lvndfyngl psnltassnp sldygfgkge iamasycsel qylanpvtsh
481 vqsaeghnqd vnsllglissr ktseavdilk lmsttflvgi cqavdlrhle enlrqtvknt
541 vsqvakkvlt tgingelhps rfcekdllkv vdreqvftyv ddpcsatypl mqrllrqvld
601 halsngetek navtsifqki gafeeelkav lpkeveaara aynggtapip nrikecrsy
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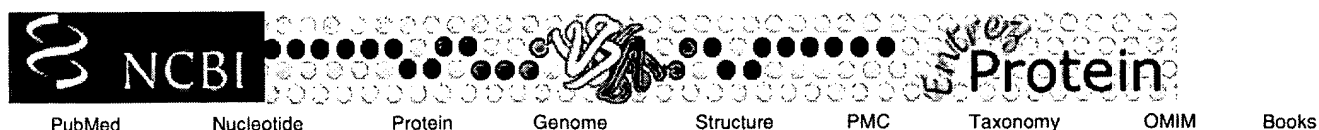
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Range: from to Features: ☐ SNP ☐ CDD ☒ MGC ☐ HPRD ☐ STS

☐ 1: [P45730](#). Reports Phenylalanine amm...[gi:1172001]

[BLink](#), [Domains](#),
[Links](#)

LOCUS P45730 715 aa linear PLN 01-MAY-2005

DEFINITION Phenylalanine ammonia-lyase.

ACCESSION P45730

VERSION P45730 GI:1172001

DBSOURCE swissprot: locus PALY_POPTR, accession [P45730](#);
class: standard.
created: Nov 1, 1995.
sequence updated: Nov 1, 1995.
annotation updated: May 1, 2005.
xrefs: [L11747.1](#), [AAA33805.1](#)
xrefs (non-sequence databases): HSSPP21310, InterProIPR008948,
InterProIPR001106, InterProIPR005922, PfamPF00221,
TIGRFAMsTIGR01226, PROSITEPS00488

KEYWORDS Lyase; Multigene family; Phenylpropanoid metabolism.

SOURCE Populus trichocarpa (Populus balsamifera subsp. trichocarpa)

ORGANISM Populus trichocarpa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.

REFERENCE 1 (residues 1 to 715)

AUTHORS Subramaniam,R., Reinold,S., Molitor,E.K. and Douglas,C.J.

TITLE Structure, inheritance, and expression of hybrid poplar (Populus
trichocarpa x Populus deltoides) phenylalanine ammonia-lyase genes

JOURNAL Plant Physiol. 102 (1), 71-83 (1993)

PUBMED 8108506

REMARK NUCLEOTIDE SEQUENCE.
STRAIN=P.trichocarpa X P.deltoides; TISSUE=Leaf

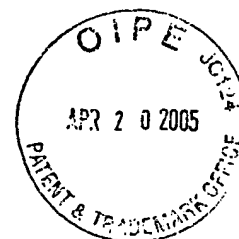
COMMENT [FUNCTION] This is a key enzyme of plant metabolism catalyzing the
first reaction in the biosynthesis from L-phenylalanine of a wide
variety of natural products based on the phenylpropane skeleton.
[CATALYTIC ACTIVITY] L-phenylalanine = trans-cinnamate + NH(3).
[PATHWAY] Phenylpropanoid biosynthesis; first step.
[SUBCELLULAR LOCATION] Cytoplasmic (Probable).
[PTM] Contains an active site 4-methylidene-imidazole-5-one (MIO),
which is formed autocatalytically by cyclization and dehydration of
residues Ala-Ser-Gly (By similarity).
[SIMILARITY] Belongs to the PAL/histidase family.

FEATURES Location/Qualifiers

source 1..715
/organism="Populus trichocarpa"
/db_xref="taxon:3694"

gene 1..715
/gene="PAL"

Protein 1..715
/gene="PAL"



Bond /product="Phenylalanine ammonia-lyase"
/EC_number="4.3.1.5"
bond(201,203)
/gene="PAL"
/bond_type="xlink"
/note="5-imidazolinone (Ala-Gly) (By similarity)."
/evidence=not_experimental

Site 202
/gene="PAL"
/site_type="modified"
/note="2,3-didehydroalanine (Ser) (By similarity)."
/evidence=not_experimental



ORIGIN

```
1 metvtknqyg ngsleslcvn qrdplswgva aeamkgshld evkrmvadyr kpvvklgget
61 ltiaqvasia ghdtgdvkve lsesarpgvk assdwvmdsm dkgtdsygvt tgfgatshrr
121 tkqggalqke lirflnagif gngtetchtl phsatraaml vrintllqgy sgirfeilea
181 itrllnnnit pclplr tit asgdlvp lsy iaglltgrpn skatgptgev ldaaeafkaa
241 giesgffelq pkeglalvng tavsglasm vlfetnvlav lsellsaifa evmngkpeft
301 dhlthklkhh pgieaaaaim ehildgsaym kaakklhetd plqkpkqdry alrtspqwlq
361 pqievirfst ksiereinsv ndnplidvsr nkaihgggnfq gtpigvsm dn vrlaiasigk
421 llfaqfselv ndfynnglps nltasrnpsl dygfkgaiea masycselq lanpvtthvq
481 saeqhnqdv n slglissrkt aeavdilklm sttflvalcq aidlrhleen lksavkntvs
541 qvskrvlttg angelhpsrf cekellkvvd reyvfayvdd pcsatyplmq klrqvfdha
601 lengeneknf stsvfqkiea feeelkallp kevesaraay dsgnsaidnk ikecrsyply
661 kfvreelgtv lltgekvqsp geefdkvfta mcqgkiidpm leclgewngs plpic
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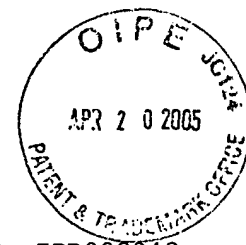
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Range: from to
 Features:
 ☐ SNP
 ☐ CDD
 ☒ MGC
 ☐ HPRD
 ☐ STS

☐ 1: [O64963](#). Reports Phenylalanine amm...[gi:6647711]

[BLink](#), [Domains](#),
[Links](#)

LOCUS 064963 717 aa linear PLN 01-MAY-2005
 DEFINITION Phenylalanine ammonia-lyase 1.
 ACCESSION 064963
 VERSION 064963 GI:6647711
 DBSOURCE swissprot: locus PAL1_PRUAV, accession [O64963](#);
 class: standard.
 created: May 30, 2000.
 sequence updated: May 30, 2000.
 annotation updated: May 1, 2005.
 xrefs: [AF036948.1](#), [AAC78457.1](#)
 xrefs (non-sequence databases): HSSPP21310, InterProIPR008948,
 InterProIPR001106, InterProIPR005922, PfamPF00221,
 TIGRFAMsTIGR01226, PROSITEPS00488
 KEYWORDS Lyase; Multigene family; Phenylpropanoid metabolism.
 SOURCE Prunus avium (sweet cherry)
 ORGANISM Prunus avium
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 REFERENCE 1 (residues 1 to 717)
 AUTHORS Wiersma, P.A. and Wu, Z.
 TITLE A full-length cDNA for phenylalanine ammonia-lyase cloned from ripe
 Sweet Cherry fruit (Prunus avium)
 JOURNAL Unpublished
 REMARK NUCLEOTIDE SEQUENCE.
 STRAIN=cv. Summit
 COMMENT [FUNCTION] This is a key enzyme of plant metabolism catalyzing the
 first reaction in the biosynthesis from L-phenylalanine of a wide
 variety of natural products based on the phenylpropane skeleton.
 [CATALYTIC ACTIVITY] L-phenylalanine = trans-cinnamate + NH(3).
 [PATHWAY] Phenylpropanoid biosynthesis; first step.
 [SUBCELLULAR LOCATION] Cytoplasmic (Probable).
 [PTM] Contains an active site 4-methylidene-imidazole-5-one (MIO),
 which is formed autocatalytically by cyclization and dehydration of
 residues Ala-Ser-Gly (By similarity).
 [SIMILARITY] Belongs to the PAL/histidase family.
 FEATURES
 source 1..717
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 /db_xref="taxon:42229"
 gene 1..717
 /gene="PAL1"
 Protein 1..717
 /gene="PAL1"
 /product="Phenylalanine ammonia-lyase 1"



Bond /EC_number="4.3.1.5"
bond(203,205)
/gene="PAL1"
/bond_type="xlink"
/note="5-imidazolinone (Ala-Gly) (By similarity)."
/evidence=not_experimental

Site 204
/gene="PAL1"
/site_type="modified"
/note="2,3-didehydroalanine (Ser) (By similarity)."
/evidence=not_experimental



ORIGIN

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1 matnsikqng hkngsvelpe lcikkdplnw gvaaetlkgs hldevkrmva eyrkpvvklg
61 gesltisqva aiathdsgvk velsesarag vkassdwvmd smskgtdsyg vttgfgatsh
121 rrtkqgaalq kelirflnag vfgstkesgh tlphqatraa mlvrintlq gysgirfeil
181 evitkflnnn vtpclplrgt itasgdlvpl syiagmltgr pnskavgpdg qtlsaaeafe
241 fvginsgffe lqpkeglalv ngtavgsgla stvlfdtnil allseilsai faevmqgkpe
301 ftdhlthklk hhpggieaaa imehildgss yvkaakklhe qdplqkpkqd ryalrtspqw
361 lgpqieviry stksiereid svndnplidv srnkahhgn fggtpigvsm dntrlaiasi
421 gklmfaqfse lvndfyngl pslsggrnp sldygfkgaie iamasycsel qflanpvtnh
481 vqsaeqhnqd vnslgliissr ktaeavdilk lmsstflval cgaidlrhle enlrntvknt
541 vsqvakrtlt tgvngelhps rfcekdllkv vdreyvfayi ddpcsatypl mqklrqvlve
601 haltngenek nastsifqki vafeeelkvl lpkevdsara aldsgsagvp nritecrsyp
661 lykfvreelg aeyltgekvr spgeedkvf taicegkiid pildclegwn gaplpic
```

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Range: from to
 Features:
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 ☒ MGC
 ☐ HPRD
 ☐ STS

☐ 1: [P45732](#). Reports Phenylalanine amm...[gi:1172002]

[BLink](#), [Domains](#),
[Links](#)

LOCUS P45732 715 aa linear PLN 01-MAY-2005
 DEFINITION Phenylalanine ammonia-lyase.
 ACCESSION P45732
 VERSION P45732 GI:1172002
 DBSOURCE swissprot: locus PALY_STYHU, accession [P45732](#);
 class: standard.
 created: Nov 1, 1995.
 sequence updated: Nov 1, 1995.
 annotation updated: May 1, 2005.
 xrefs: [L36822.1](#), [AAA99500.1](#)
 xrefs (non-sequence databases): [HSSPP21310](#), [InterProIPR008948](#),
[InterProIPR001106](#), [InterProIPR005922](#), [PfamPF00221](#),
[TIGRFAMsTIGR01226](#), [PROSITEPS00488](#)
 KEYWORDS Lyase; Phenylpropanoid metabolism.
 SOURCE Stylosanthes humilis (Townsville stylo)
 ORGANISM *Stylosanthes humilis*
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
 Aeschynomeneae; Stylosanthes.
 REFERENCE 1 (residues 1 to 715)
 AUTHORS Manners,J.M., McIntyre,C.L. and Nourse,J.P.
 TITLE Cloning and sequence of a cDNA encoding phenylalanine ammonia-lyase
 from the tropical forage legume *Stylosanthes humilis*
 JOURNAL Plant Physiol. 108 (3), 1301-1302 (1995)
 PUBMED 7630950
 REMARK NUCLEOTIDE SEQUENCE.
 STRAIN=cv. Paterson; TISSUE=Stem
 COMMENT [FUNCTION] This is a key enzyme of plant metabolism catalyzing the
 first reaction in the biosynthesis from L-phenylalanine of a wide
 variety of natural products based on the phenylpropane skeleton.
 [CATALYTIC ACTIVITY] L-phenylalanine = trans-cinnamate + NH(3).
 [PATHWAY] Phenylpropanoid biosynthesis; first step.
 [SUBCELLULAR LOCATION] Cytoplasmic (Probable).
 [PTM] Contains an active site 4-methylidene-imidazole-5-one (MIO),
 which is formed autocatalytically by cyclization and dehydration of
 residues Ala-Ser-Gly (By similarity).
 [SIMILARITY] Belongs to the PAL/histidase family.
 FEATURES
 source Location/Qualifiers
 1..715
 /organism="Stylosanthes humilis"
 /db_xref="taxon:35628"
 gene 1..715
 /gene="PAL17.1"
 Protein 1..715

Bond /gene="PAL17.1"
/product="Phenylalanine ammonia-lyase"
/EC_number="4.3.1.5"
bond(201,203)
/gene="PAL17.1"
/bond_type="xlink"
/note="5-imidazolinone (Ala-Gly) (By similarity)."
/evidence=not_experimental

Site 202
/gene="PAL17.1"
/site_type="modified"
/note="2,3-didehydroalanine (Ser) (By similarity)."
/evidence=not_experimental



ORIGIN

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1 mdthanadat fcltanngqq prhdplnwaa aaealkgshl devkrmvsey rkplvnlggq
61 tltisqvaaai aandqgvsvq lseasragvk assdwvmdsm nngtdsygvt tgfgatshrr
121 tkqggalqke lirflnagif gngtetnctl phtatraaml vrintllqgy sgirfeilea
181 itkllnnnit pclplrgtit asgdlvpls y iaglltgrpn skavgpnget lnakeafqaa
241 gigsdffelq pkeglalvng tpgvsglasv vlfeanilav lsevlsaifa evmqgkpeft
301 dhlthklkhh pgqieaaaam ehildgssyv kaakklheid plqkpkqdry alrtspqwlq
361 plvevirfst ksiereinsv ndnplidvsr nkalhggnfq gtpigvsmndn trlavasigk
421 lmfaqfselv ndfyngnpls nlsasrnpsl dygfkgtcia masycselqy lanpvtshvq
481 saeqhnqdv n slglisarkt neaveilkml sptylialcq aidlrhleen lkntvkntvs
541 qvakrtlittg vngelhpsrf cekdllkiyd reycfayidd pcsatyplmq klrqvlveha
601 lanaeneknv ntsifqkitt feeelktllp kevegariay enggsaipnk ikecrsyply
661 kfvreelgte mltgekvrrsp geecdklfta mcqgkiidpl lecigewnga plplc
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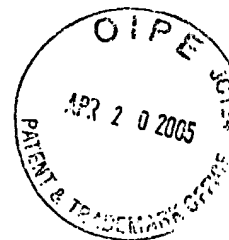
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 ☐ HPRD
 ☐ STS

☐ 1: [P45734](#). Reports Phenylalanine amm...[gi:1172003]

[BLink](#), [Domains](#),
[Links](#)

LOCUS P45734 725 aa linear PLN 01-MAY-2005
 DEFINITION Phenylalanine ammonia-lyase.
 ACCESSION P45734
 VERSION P45734 GI:1172003
 DBSOURCE swissprot: locus PALY_TRISU, accession [P45734](#);
 class: standard.
 created: Nov 1, 1995.
 sequence updated: Nov 1, 1995.
 annotation updated: May 1, 2005.
 xrefs: [M91192.1](#), [AAA17993.1](#)
 xrefs (non-sequence databases): [HSSPP21310](#), [InterProIPR008948](#),
[InterProIPR001106](#), [InterProIPR005922](#), [PfamPF00221](#),
[TIGRFAMsTIGR01226](#), [PROSITEPS00488](#)
 KEYWORDS Lyase; Multigene family; Phenylpropanoid metabolism.
 SOURCE Trifolium subterraneum
 ORGANISM Trifolium subterraneum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Trifolium.
 REFERENCE 1 (residues 1 to 725)
 AUTHORS Howles,P.A., Arioli,T. and Weinman,J.J.
 TITLE Characterization of a phenylalanine ammonia-lyase multigene family
 in Trifolium subterraneum
 JOURNAL Gene 138 (1-2), 87-92 (1994)
 PUBMED [8125321](#)
 REMARK NUCLEOTIDE SEQUENCE.
 STRAIN=cv. Karridale; TISSUE=Leaf
 COMMENT [FUNCTION] This is a key enzyme of plant metabolism catalyzing the
 first reaction in the biosynthesis from L-phenylalanine of a wide
 variety of natural products based on the phenylpropane skeleton.
 [CATALYTIC ACTIVITY] L-phenylalanine = trans-cinnamate + NH(3).
 [PATHWAY] Phenylpropanoid biosynthesis; first step.
 [SUBCELLULAR LOCATION] Cytoplasmic (Probable).
 [PTM] Contains an active site 4-methylidene-imidazole-5-one (MIO),
 which is formed autocatalytically by cyclization and dehydration of
 residues Ala-Ser-Gly (By similarity).
 [SIMILARITY] Belongs to the PAL/histidase family.
 FEATURES
 source Location/Qualifiers
 1..725
 /organism="Trifolium subterraneum"
 /db_xref="taxon:3900"
 gene 1..725
 /gene="PAL1"
 Protein 1..725



Bond /gene="PAL1"
/product="Phenylalanine ammonia-lyase"
/EC_number="4.3.1.5"
bond(211,213)
/gene="PAL1"
/bond_type="xlink"
/note="5-imidazolinone (Ala-Gly) (By similarity)."
/evidence=not_experimental

Site 212
/gene="PAL1"
/site_type="modified"
/note="2,3-didehydroalanine (Ser) (By similarity)."
/evidence=not_experimental

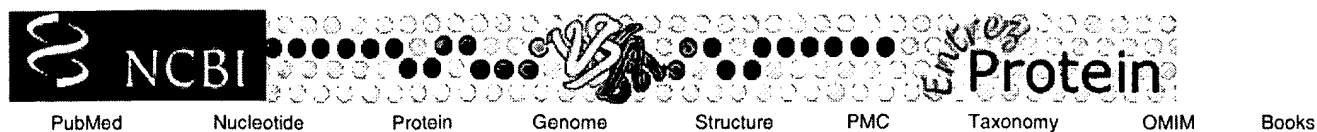
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1 mevvaaailk nnindydsfc lthanannmk vnaadplnwg vaaeamkgsh ldevkrmvee
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121 tgfgatshrr tkqggalqke lirflnagif gngtesnhtl phtatraaml vrintllqgy
181 sgirfeilea itklennnit pclplrgtit asgdlvplsy iaglltgrsn skahgpsgem
241 lnakeafqla ginaeffelq pkeglalvng tavgsylasi vlfeanilav lsevlsaifa
301 evmvgkpeft dhlthklkhh pgqieaaaam ehilhgsayv kdakklhemd plqkpkqdry
361 alrtspqwlq plievirfst ksiereinsv ndnplidvsv nkalhggnfq gtpigvsmdn
421 trlalasigk llfaqfselv ndfynnglps nlsasrnpsl dygfkgsaia masycselqy
481 lanpvtthvq saeqhngdvn slglissrkt keaieilqlm sstflialcq aidlrhleen
541 lknsvkntvs qvakktltig vsgelhpsrf cekdllkvvd rehvfisyidd pcsatyplaq
601 klrqvlvdha lvngesekns ntsifqkiat feeelktllp kevesartay engnstiank
661 ingcrsyply kfvreelgts lltgervisp geecdklfta mcqgkiidpl lkclgewnga
721 plpic
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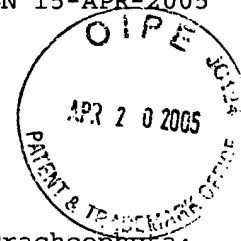
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☐ 1: [CAA05251](#). Reports phenylalanine amm...[gi:2631995]

BLink, Domains,
Links

LOCUS CAA05251 713 aa linear PLN 15-APR-2005
 DEFINITION phenylalanine ammonia lyase [Digitalis lanata].
 ACCESSION CAA05251
 VERSION CAA05251.1 GI:2631995
 DBSOURCE embl locus DLJ002221, accession [AJ002221.1](#)
 KEYWORDS .
 SOURCE Digitalis lanata
 ORGANISM Digitalis lanata
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiids; Lamiales; Plantaginaceae; Digitalideae;
 Digitalis.
 REFERENCE 1 (residues 1 to 713)
 AUTHORS Thoeringer,C.
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 713)
 AUTHORS Thoeringer,C.
 TITLE Direct Submission
 JOURNAL Submitted (14-NOV-1997) Thoeringer C., Institute of Pharmaceutical
 Biology, Martin-Luther-University Halle, Hoher Weg 7, D-06120,
 GERMANY



FEATURES Location/Qualifiers
 source 1..713
 /organism="Digitalis lanata"
 /db_xref="taxon:49450"
 /clone_lib="Lambda ZAP"
 /dev_stage="leaves"
Protein 1..713
 /product="phenylalanine ammonia lyase"
CDS 1..713
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 /db_xref="GOA:O23924"
 /db_xref="InterPro:IPR001106"
 /db_xref="InterPro:IPR005922"
 /db_xref="InterPro:IPR008948"
 /db_xref="UniProt/Swiss-Prot:O23924"

ORIGIN

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1  maavvenghh  gnngfcvkqn  dplnwvaae  elkgshldev  krmveefrkt  vvklggetlt
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121  ggalqkelir  flnagifgng  testhtlphs  atraamlvri  ntllqgysgi  rfeiletitk
181  flnhnitpcl  plrgtitasg  dlvpplsiai  lltgrpnksa  vgpngeslna  eqafklagan
241  sgloffelqpk  eglalvngta  vsgglasial  yeailslla  evmsavfaev  mngkpeftdh
301  lthklkhpg  qieaaaimeh  ildgssyvka  aqkmhemdpl  qkpkqdryal  rtspqwlgrpq
361  ievirtatkm  iereinsvnd  nplidvsrnk  alhggnfqgt  pigvsmdnsr  laiasigklm
421  faqfselvnd  fynnglpsnl  sggrnpsldy  gfkqseiam  sycselqla  npvtnhqvsa



```

481 eqhnqdvnsI glissrktve aldilklmss tylvalcqi dlrhleenlr lsvkntisqv
541 akrtlttgvn gelhpsrfce ldllrvvdre yvfayvddpc satypImqkl rqvIvehalk
601 ngeneknast sifqkieafe aelkavlpke vesarvaled gkpaianrit ecrsyplykf
661 ireelgtnfl tgekvmSPge ecdrvftams kglivdpllk clegwngapl pic

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☐ 1: CAA37129. Reports phenylalanine amm...[gi:18377]

BLink, Domains,
Links

LOCUS CAA37129 713 aa linear PLN 18-AUG-1993
 DEFINITION phenylalanine ammonia-lyase [Glycine max].
 ACCESSION CAA37129
 VERSION CAA37129.1 GI:18377
 DBSOURCE embl locus DMPAL1, accession [X52953.1](#)
 KEYWORDS .
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 REFERENCE 1 (residues 1 to 713)
 AUTHORS Frank,R.L. and Vodkin,L.O.
 TITLE Sequence and structure of a phenylalanine ammonia-lyase gene from
 Glycine max
 JOURNAL DNA Seq. 1 (5), 335-346 (1991)
 PUBMED [1799682](#)
 REFERENCE 2 (residues 1 to 713)
 AUTHORS Frank,R.L.
 TITLE Direct Submission
 JOURNAL Submitted (07-MAY-1990) Frank R.L., University of Missouri-Rolla,
 Life Sciences Department, 105 Schrenk Hall, Rolla, Missouri 65401,
 U.S.A

FEATURES Location/Qualifiers
 source 1..713
 /organism="Glycine max"
 /strain="T225"
 /db_xref="taxon:3847"
 /clone="lambda P10"
 /tissue_type="leaf"
 /clone_lib="lambda charon 35"
 Protein 1..713
 /product="phenylalanine ammonia-lyase"
 /EC_number="4.3.1.5"
 CDS 1..713
 /gene="PAL1"
 /coded_by="join(X52953.1:189..580,X52953.1:2100..3849)"
 /db_xref="GOA:P27991"
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ORIGIN

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 121 qggalqkeli rflnagifgn gtessthlph tatraamlvr intllogysg irfeileait
 181 kllnnvtpc ldlrgtitas gdlvplsya glltgrpsnk avgpsgevl nakeafelasi

241 nseffelqpk eglalvngta vsgglasmvl feanilavls evlsaifaev mggkpeftdh
301 lthklkhpg qieaaaimeh ildgssymka akklheidpl qkpkqdryal rtspqwlgpl
361 ievirfstks iereinsvnd nplidvsrnk alhggmfqgt pigvsmdntr lalasigklm
421 faqfselvnd fynnglpsnl tasrnpsldy gfkgaieama sycselqyla npvtthvqsa
481 eqhnqdvns glissrktne aieilklmss tflialcqai dlrhleenlk nsvkntvsqv
541 skrilttgvn gelhpsrfce kdllkvvdre yifsyiddpc satyplmqkl rqvldhalv
601 naeekdvns sifqkiaife eelknllpke vegaraayes gkaaipnkiq ecrsyplykf
661 vreelgtgll tgekvrspe efdklftamc qgkiidplme clgewngapl pis

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